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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2009; month=4; day=23; hr=15; min=31; sec=6; ms=776;]
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Application No: 10541752   Version No: 1.0

Input Set:

Output Set:

Started: 2009-04-13 14:03:05.576

Finished: 2009-04-13 14:03:05.888

Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 312 ms

Total Warnings: 2

Total Errors: 0

No. of SeqIDs Defined: 2

Actual SeqID Count: 2

Error code   Error Description

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<110>   Ikeda, Keiko

<120>   Cytoplasmic Polyhedrosis Virus Protein Complex of a Polyhedrin
         and a VP3 Polypeptide

<130>   052777

<140>   10541752
<141>   2009-04-13

<150>   PCT/JP2004/000032
<151>   2005-07-10

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<170>   PatentIn version 3.5

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<211>   3259
<212>   DNA
<213>   Bombyx mori cytoplasmic polyhedrosis virus (strain H)

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gcgttcagtt catctattac acgtacgctc ggaagacaac acgctacgtt acaactggat   360

gttaggtgtg tacgcgcgct caactaatta cactcacacca gtcggacagt tggtagttaa   420

tgcgccagcg attctcaact attctaatcc gcaagatgca ttcaatagtg tatttgtagc   480

gttaggtata gactacattg ataccgat aactaacagc aacatctttg acgacagttc   540

gacaccctat aatgttcgta tttggcatgc ccctactatg acggaggtta accatatcct   600

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taactcctat gaggaccaga gttttgagtc catgttcggt gagactatat cggtagtgac      1920

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taaactgatg acatatgctt taatacgaga gcagatatca ttaactgaaa acatgactca      2580

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tatatatcta tttatcgcag taatcatgaa tgaaccaaat ggagcagcta ctcccgccag      2820

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gctcgttgaa gcagacgtga cgttgatgtt acgcgatatc ggcataacac atgagataat      3060

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ggggtgggaa acgttagcc                                               3259



<210>  2
<211>  1057
<212>  PRT
<213>  Bombyx mori cytoplasmic polyhedrosis virus (strain H)

<400>  2

Met Trp His Tyr Thr Ser Ile Asn Asn Asp Thr Arg Val Ala Leu Asp
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Pro Lys Pro Asn Gln Ile Arg Thr Ile Thr Lys Pro Asn Thr Val Pro
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Gln Leu Gly Thr Asp Tyr Leu Tyr Thr Phe Asn Ser Gln Arg Arg Ser
        35                  40                  45


His Thr Leu Arg Leu Leu Gly Pro Phe Gln Tyr Phe Asn Phe Ser Glu
    50                  55                  60


Thr Asp Arg Gly His Pro Leu Phe Arg Leu Pro Leu Lys Tyr Pro Ser
65                  70                  75                  80


Lys Ala Ile Pro Ala Asp Glu Leu Ile Asp Asn Leu His Ser Trp Met
                85                  90                  95


Arg Ser Val His Leu Leu His Val Arg Ser Glu Asp Asn Thr Leu Arg
                100                 105                 110
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Tyr Asn Trp Met Leu Gly Val Tyr Ala Arg Ser Thr Asn Tyr Thr Thr
        115   120   125

Pro Val Gly Gln Leu Val Val Asn Ala Pro Ala Ile Leu Asn Tyr Ser
        130   135   140

Asn Pro Gln Asp Ala Phe Asn Ser Val Phe Val Ala Leu Gly Ile Asp
145   150   155   160

Tyr Ile Asp Ile Pro Ile Thr Asn Ser Asn Ile Phe Asp Asp Ser Ser
                165   170   175

Thr Pro Tyr Asn Val Arg Ile Trp His Ala Pro Thr Met Thr Glu Val
                180   185   190

Asn His Ile Leu Ala Leu Met Arg Lys Ser Thr Leu Val Ser Thr His
        195   200   205

Ser Ser Trp His Trp Asp Val Leu His Thr Phe His Tyr Arg Ser Glu
        210   215   220

Ser Asp Met Ile Asp His Phe Ala Ala Lys Ile Leu Glu Asp Trp Arg
225   230   235   240

Gln Lys Glu Lys Leu Asp Lys Gly Ala Leu Val Glu Ala Asp Arg Val
                245   250   255

Val Gln Arg Leu Ile Pro Leu Ser Ser Ser Thr Tyr Val Gln Arg Leu
                260   265   270

Ala Ala Ile Gly Ala Leu Tyr Pro Asn Glu Phe Thr Glu Asn Val Leu
        275   280   285

Asp Leu Ser Arg Leu Ser Thr Ala Leu Leu Gln Leu Ser Asp Thr Tyr
        290   295   300

Tyr Gln His Ala Asn Asp Gln Leu Arg Arg Leu Tyr Arg Arg Met Tyr
305   310   315   320

Asn Asp Ser Arg Thr Leu Tyr Met Thr Gln Arg His Gln Glu Leu Leu
                325   330   335

Leu Ala Gln Ile Thr Ala Asp Pro Asn Ile Leu Leu Tyr Pro Tyr Thr
        340   345   350

Tyr Ile Phe Thr Thr Ala Tyr Thr Ser Met Asn Tyr Ile Ser Asn Thr
        355   360   365

Gly Gln Gly Arg Ile Lys His Ser Leu Ala Val Thr Gly Thr Thr Glu
        370   375   380

His Thr Ile Ala Asp Ile Thr Leu Gly Pro Met Ser Glu Asp Val Val
385   390   395   400

Thr Ile Ser Met Val Glu Pro Met Ser Ile Ala Ala Glu Asp Met Tyr
                405   410   415

Gly Tyr Val Leu Asp Thr Pro Thr Arg Asp Ile Trp Pro Ala Asp Glu
                420   425   430

Gln Ile Glu Gln Lys Gly Asp Ala Val Ala Leu Tyr Asp Thr Lys Thr
        435   440   445

Ser Arg Ala Leu Gly Met Phe Asn Asn Thr Val Arg Ile Asp Asp Leu
        450   455   460

Leu Ser Pro Leu Leu Gly Leu Val Tyr Arg Thr Tyr Ile Lys Gly Asp
465   470   475   480

Thr Met Thr Met Thr Gln Gly Ser Leu Asp His Leu Thr Leu Cys Ala
                485   490   495

Ala Val Asp Ser Asp Ile Thr Phe Val Gly Asn Arg Met Ile Ala Pro
                500   505   510

Leu Ala Glu Gly Tyr Ile Pro Lys Ala Met His Arg Asn Asn Ser Thr
        515   520   525

Met Lys Met Leu Ser Leu Tyr Val Ala Leu Lys Lys Leu Glu Asn Phe
        530   535   540

Thr Thr Asn Ser Tyr Leu Met Ala Pro Asp Thr Ser Ile Ile Leu Leu
545   550   555   560

Gly Ala Glu Arg Glu Pro Ala Val Ser Ile Leu Arg Arg Phe Asn Arg

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                565                      570                      575


Ser Val Ser Asn Val Arg Ile Ile Gly Met Gly Asp Arg Ala Val Glu
            580                      585                      590


Pro Asn Ile Arg Val Arg Val Pro Phe Pro Ile Asp Lys Asn Ile Ser
            595                      600                      605


Ala Asp Phe Ile Ile Cys Asp Ile Asn Ser Tyr Glu Asp Gln Ser Phe
            610                      615                      620


Glu Ser Met Phe Gly Glu Thr Ile Ser Val Val Thr Thr Cys Ala Ser
625                      630                      635                      640


Ala Ala Thr Arg Val Leu Val Lys Ile Asn His Pro Ser Glu Tyr Met
            645                      650                      655


Ile Asn Ser Val Ile Glu Arg Leu Ser Gln Leu Gly Gly Val Phe Tyr
            660                      665                      670


His Thr Ala Leu Leu Lys Thr Ala Ser Gln Asn Pro Tyr Ser Tyr Glu
            675                      680                      685


Thr Tyr Ile Tyr Ile Thr Pro Ile Ala Ala Ala Val Arg Phe Pro Phe
            690                      695                      700


Tyr Ser Asn Ser Ala Ile Ile Asn Arg Tyr Met Thr Ala Val Ala Asp
705                      710                      715                      720


Asp Glu Thr Pro Ile Ile Pro Ser Ile His Thr Val Ile Lys Gly His
            725                      730                      735


Ser Asn Thr Tyr Ser Pro Gly Leu Phe Cys Gly Cys Ile Asp Val Gln
            740                      745                      750


Ser Ala Pro Phe Ala Leu Ser Gln Leu Lys Ser Tyr Cys Ser Glu Ala
            755                      760                      765


Thr Thr Trp Arg Val Asp Ser Asp Asp Asn Leu Val Asn Ile Ile Ala
            770                      775                      780


Arg Ile Asp Pro Ala Arg Ile Ala Leu Glu Phe Arg Thr Arg Ser Asn
785                      790                      795                      800
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Thr Ser Ala Tyr His Glu Tyr Gln Arg Tyr Val Pro Asn Gly Leu Gly
              805   810   815

Phe Lys Gly Arg Lys Thr Arg Glu Phe Arg Tyr Ile His Arg Glu Val
              820   825   830

Thr Phe Ile His Lys Leu Met Thr Tyr Ala Leu Ile Arg Glu Gln Ile
          835   840   845

Ser Leu Thr Glu Asn Met Thr Gln Val Val Ser Ile Gly Gly Arg Asn
     850   855   860

Leu Ala Asp Ile Ser Val Val Pro Leu Asn Met Lys Tyr Val Val Ile
865   870   875   880

Asp Pro Ala Thr Arg Ile Glu Thr Leu Thr Gln Glu Lys Lys Asn Ile
              885   890   895

Glu Val Gln Ser Arg Pro Phe Ser Phe Asp Ala Ala Ser Met Asp Leu
          900   905   910

Glu Asn Asn Ser Ile Tyr Leu Phe Ile Ala Val Ile Met Asn Glu Pro
          915   920   925

Asn Gly Ala Ala Thr Pro Ala Arg Thr Gln Met Asp Lys Ile Arg Asn
     930   935   940

Val Ala Thr Ala Met Leu Thr Arg Thr Asn Cys Val Ala Tyr Ile Ser
945   950   955   960

Phe Tyr Glu Ala Gly Ile Ile Thr Arg Leu Asp Gln Ser Thr Ala His
              965   970   975

Lys Thr Ile Arg Val Glu Glu Gly Arg Leu Lys Val Ala Asn Tyr Val
          980   985   990

Pro Val Asp Thr Leu Val Glu Ala Asp Val Thr Leu Met Leu Arg Asp
          995   1000   1005

Ile Gly Ile Thr His Glu Ile Ile Arg Pro Ser Thr Pro Glu Leu
     1010   1015   1020

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Ile Asn   Ala Cys Ser Asn Tyr   Gly Ile Arg Leu Gly   Ser Thr Gly
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Gly Ala   Val Leu Asp Val Phe   Asn His Tyr Ser Pro   Val Ile Lys
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Leu Val   Arg Ser
      1055
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